



1600

RAW SEQUENCE LISTING DATE: 09/20/2004
 PATENT APPLICATION: US/09/456,306A TIME: 16:09:01

Input Set : A:\021123-0265182.ST25.txt
 Output Set: N:\CRF4\09202004\I456306A.raw

3 <110> APPLICANT: DEGUSSA AG
 5 <120> TITLE OF INVENTION: NOVEL NUCLEOTIDE SEQUENCES CODING FOR THE *poxB* GENE
 7 <130> FILE REFERENCE: 021123-0265182
 9 <140> CURRENT APPLICATION NUMBER: US 09/456,306A
 10 <141> CURRENT FILING DATE: 1999-12-08
 12 <150> PRIOR APPLICATION NUMBER: DE 199 51 975.7
 13 <151> PRIOR FILING DATE: 1999-10-28
 15 <160> NUMBER OF SEQ ID NOS: 5
 17 <170> SOFTWARE: PatentIn version 3.3
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 2160
 21 <212> TYPE: DNA
 22 <213> ORGANISM: *Corynebacterium glutamicum*
 25 <220> FEATURE:
 26 <221> NAME/KEY: -35_signal
 27 <222> LOCATION: (227)..(232)
 29 <220> FEATURE:
 30 <221> NAME/KEY: -10_signal
 31 <222> LOCATION: (256)..(261)
 33 <220> FEATURE:
 34 <221> NAME/KEY: CDS
 35 <222> LOCATION: (327)..(2063)
 37 <400> SEQUENCE: 1
 38 ttagaggcga ttctgtgagg tcacttttg tggggtcggg gtctaaattt ggccagttt 60
 40 cgaggcgacc agacaggcgt gcccacatg tttaaatagg cgatcggtgg gcatctgtgt 120
 42 ttgggttcga cgggctgaaa ccaaaccaga ctgcccagca acgacggaaa tcccaaagt 180
 44 gggcatccct gtttggtacc gagtaccac ccgggcctga aactccctgg caggcggcgc 240
 46 aagcgtggca acaactggaa tttaagagca caattgaagt cgcaccaagt taggcaacac 300
 48 aatagccata acgttgagga gttcaag atg gca cac agc tac gca gaa caa tta 353
 49 Met Ala His Ser Tyr Ala Glu Gln Leu
 50 1 5
 52 att gac act ttg gaa gct caa ggt gtg aag cga att tat ggt ttg gtg 401
 53 Ile Asp Thr Leu Glu Ala Gln Gly Val Lys Arg Ile Tyr Gly Leu Val
 54 10 15 20 25
 56 ggt gac agc ctt aat ccg atc gtg gat gct gtc cgc caa tca gat att 449
 57 Gly Asp Ser Leu Asn Pro Ile Val Asp Ala Val Arg Gln Ser Asp Ile
 58 30 35 40
 60 gag tgg gtg cac gtt cga aat gag gaa gcg gcg ttt gca gcc ggt 497
 61 Glu Trp Val His Val Arg Asn Glu Glu Ala Ala Ala Phe Ala Ala Gly
 62 45 50 55
 64 gcg gaa tcg ttg atc act ggg gag ctg gca gta tgt gct gct tct tgt 545
 65 Ala Glu Ser Leu Ile Thr Gly Glu Leu Ala Val Cys Ala Ala Ser Cys
 66 60 65 70



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68	ggc	cct	gga	aac	aca	cac	ctg	att	cag	ggc	ctt	tat	gat	tcg	cat	cga	593
69	Gly	Pro	Gly	Asn	Thr	His	Leu	Ile	Gln	Gly	Leu	Tyr	Asp	Ser	His	Arg	
70	75				80						85						
72	aat	ggc	aag	gtg	ttg	gcc	atc	gct	agc	cat	att	ccg	agt	gcc	cag	641	
73	Asn	Gly	Ala	Lys	Val	Leu	Ala	Ile	Ala	Ser	His	Ile	Pro	Ser	Ala	Gln	
74	90				95						100					105	
76	att	ggc	tcg	acg	ttc	ttc	cag	gaa	acg	cat	ccg	gag	att	ttg	ttt	aag	689
77	Ile	Gly	Ser	Thr	Phe	Phe	Gln	Glu	Thr	His	Pro	Glu	Ile	Leu	Phe	Lys	
78					110					115			120				
80	gaa	tgc	tct	ggc	tac	tgc	gag	atg	gtg	aat	ggc	gag	cag	ggc	gaa	737	
81	Glu	Cys	Ser	Gly	Tyr	Cys	Glu	Met	Val	Asn	Gly	Gly	Glu	Gln	Gly	Glu	
82		125				130				135							
84	cgc	att	ttg	cat	cac	gca	att	cag	tcc	acc	atg	gca	ggc	ggc	aaa	ggc	785
85	Arg	Ile	Leu	His	His	Ala	Ile	Gln	Ser	Thr	Met	Ala	Gly	Lys	Gly	Val	
86		140				145					150						
88	tcg	gtg	gta	gtg	att	cct	ggc	atc	gct	aag	gaa	gac	gca	ggc	gac	833	
89	Ser	Val	Val	Val	Ile	Pro	Gly	Asp	Ile	Ala	Lys	Glu	Asp	Ala	Gly	Asp	
90		155				160				165							
92	ggc	act	tat	tcc	aat	tcc	act	att	tct	tct	ggc	act	cct	gtg	gtg	ttc	881
93	Gly	Thr	Tyr	Ser	Asn	Ser	Thr	Ile	Ser	Ser	Gly	Thr	Pro	Val	Val	Phe	
94		170				175				180			185				
96	ccg	gat	cct	act	gag	gct	gca	gca	ctg	gtg	gag	gca	ggc	att	aac	aac	929
97	Pro	Asp	Pro	Thr	Glu	Ala	Ala	Leu	Val	Glu	Ala	Ile	Asn	Asn	Ala		
98					190					195			200				
100	aag	tct	gtc	act	ttg	ttc	tgc	ggc	ggc	gtg	aag	aat	gct	ccg	ggc	977	
101	Lys	Ser	Val	Thr	Leu	Phe	Cys	Gly	Ala	Gly	Val	Lys	Asn	Ala	Arg	Ala	
102		205				210					215						
104	cag	gtg	ttg	gag	ttg	gca	ggc	gag	att	aaa	tca	ccg	atc	ggg	cat	ggc	1025
105	Gln	Val	Leu	Glu	Leu	Ala	Glu	Lys	Ile	Lys	Ser	Pro	Ile	Gly	His	Ala	
106		220				225				230							
108	ctg	ggc	ttt	gag	ttt	gca	ggc	gag	aat	ccg	ttt	gag	gtc	ggc	ttt	1073	
109	Leu	Gly	Lys	Gln	Tyr	Ile	Gln	His	Glu	Asn	Pro	Phe	Glu	Val	Gly		
110		235				240				245							
112	atg	tct	ggc	ctg	ttt	gtt	acg	cat	gag	aat	ccg	ttt	gag	gtc	ggc	ttt	1121
113	Met	Ser	Gly	Leu	Leu	Gly	Tyr	Gly	Ala	Cys	Val	Asp	Ala	Ser	Asn	Glu	
114		250				255				260			265				
116	ggc	gat	ctg	ctg	att	cta	ttt	gtt	acg	gat	ttc	cct	tat	tct	gat	ttc	1169
117	Ala	Asp	Leu	Leu	Ile	Leu	Gly	Thr	Asp	Phe	Pro	Tyr	Ser	Asp	Phe		
118					270					275			280				
120	ctt	cct	aaa	gac	aac	gtt	gcc	cag	gtg	gat	atc	aac	ggc	cac	att	1217	
121	Leu	Pro	Lys	Asp	Asn	Val	Ala	Gln	Val	Asp	Ile	Asn	Gly	Ala	His	Ile	
122		285				290					295						
124	ggc	cgt	acc	acg	gtg	aag	tat	ccg	gtg	acc	ggc	gat	gtt	gct	gca	1265	
125	Gly	Arg	Arg	Thr	Thr	Val	Lys	Tyr	Pro	Val	Thr	Gly	Asp	Val	Ala	Ala	
126		300				305					310						
128	aca	atc	gaa	aat	att	ttt	cct	cat	gtg	aag	gaa	aaa	aca	gat	cgt	tcc	1313
129	Thr	Ile	Glu	Asn	Ile	Leu	Pro	His	Val	Lys	Glu	Lys	Thr	Asp	Arg	Ser	
130		315				320					325						
132	tcc	ctt	gat	cgg	atg	ctc	aag	gca	cac	gag	cgt	aag	ttt	agc	tcg	gtg	1361

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133	Phe	Leu	Asp	Arg	Met	Leu	Lys	Ala	His	Glu	Arg	Lys	Leu	Ser	Ser	Val	
134	330				335					340						345	
136	gta	gag	acg	tac	aca	cat	aac	gtc	gag	aag	cat	gtg	cct	att	cac	cct	1409
137	Val	Glu	Thr	Tyr	Thr	His	Asn	Val	Glu	Lys	His	Val	Pro	Ile	His	Pro	
138								350			355					360	
140	gaa	tac	gtt	gcc	tct	att	ttg	aac	gag	ctg	gcg	gat	aag	gat	gcg	gtg	1457
141	Glu	Tyr	Val	Ala	Ser	Ile	Leu	Asn	Glu	Leu	Ala	Asp	Lys	Asp	Ala	Val	
142								365			370					375	
144	ttt	act	gtg	gat	acc	ggc	atg	tgc	aat	gtg	tgg	cat	gcg	agg	tac	atc	1505
145	Phe	Thr	Val	Asp	Thr	Gly	Met	Cys	Asn	Val	Trp	His	Ala	Arg	Tyr	Ile	
146							380			385						390	
148	gag	aat	ccg	gag	gga	acg	cgc	gac	ttt	gtg	ggt	tca	ttc	cgc	cac	ggc	1553
149	Glu	Asn	Pro	Glu	Gly	Thr	Arg	Asp	Phe	Val	Gly	Ser	Phe	Arg	His	Gly	
150							395			400						405	
152	acg	atg	gct	aat	gcg	ttg	cct	cat	gcg	att	ggt	gcg	caa	agt	gtt	gat	1601
153	Thr	Met	Ala	Asn	Ala	Leu	Pro	His	Ala	Ile	Gly	Ala	Gln	Ser	Val	Asp	
154							410			415						425	
156	cga	aac	cgc	cag	gtg	atc	gcg	atg	tgt	ggc	gat	ggt	ggt	ttg	ggc	atg	1649
157	Arg	Asn	Arg	Gln	Val	Ile	Ala	Met	Cys	Gly	Asp	Gly	Gly	Leu	Gly	Met	
158							430			435						440	
160	ctg	ctg	ggt	gag	ctt	ctg	acc	gtt	aag	ctg	cac	caa	ctt	ccg	ctg	aag	1697
161	Leu	Leu	Gly	Glu	Leu	Leu	Thr	Val	Lys	Leu	His	Gln	Leu	Pro	Leu	Lys	
162							445			450						455	
164	gct	gtg	gtg	ttt	aac	aac	agt	tct	ttg	ggc	atg	gtg	aag	ttg	gag	atg	1745
165	Ala	Val	Val	Phe	Asn	Asn	Ser	Ser	Leu	Gly	Met	Val	Lys	Leu	Glu	Met	
166							460			465						470	
168	ctc	gtg	gag	gga	cag	cca	gaa	ttt	ggt	act	gac	cat	gag	gaa	gtg	aat	1793
169	Leu	Val	Glu	Gly	Gln	Pro	Glu	Phe	Gly	Thr	Asp	His	Glu	Glu	Val	Asn	
170							475			480						485	
172	ttc	gca	gag	att	gcg	gcg	gct	gcg	ggt	atc	aaa	tcg	gta	cgc	atc	acc	1841
173	Phe	Ala	Glu	Ile	Ala	Ala	Ala	Ala	Gly	Ile	Lys	Ser	Val	Arg	Ile	Thr	
174							490			495						505	
176	gat	ccg	aag	aaa	gtt	ccg	gag	cag	cta	gct	gag	gca	ttg	gca	tat	cct	1889
177	Asp	Pro	Lys	Lys	Val	Arg	Glu	Gln	Leu	Ala	Glu	Ala	Leu	Ala	Tyr	Pro	
178							510			515						520	
180	gga	cct	gta	ctg	atc	gat	atc	gtc	acg	gat	cct	aat	gcg	ctg	tcg	atc	1937
181	Gly	Pro	Val	Leu	Ile	Asp	Ile	Val	Thr	Asp	Pro	Asn	Ala	Leu	Ser	Ile	
182							525			530						535	
184	cca	cca	acc	atc	acg	tgg	gaa	cag	gtc	atg	gga	ttc	agc	aag	gcg	gcc	1985
185	Pro	Pro	Thr	Ile	Thr	Trp	Glu	Gln	Val	Met	Gly	Phe	Ser	Lys	Ala	Ala	
186							540			545						550	
188	acc	cga	acc	gtc	ttt	ggt	gga	gga	gta	gga	gca	atg	atc	gat	ctg	gcc	2033
189	Thr	Arg	Thr	Val	Phe	Gly	Gly	Val	Gly	Ala	Met	Ile	Asp	Leu	Ala		
190							555			560						565	
192	cgt	tcg	aac	ata	agg	aat	att	cct	act	cca	tgatgattga	tacacctgct					2083
193	Arg	Ser	Asn	Ile	Arg	Asn	Ile	Pro	Thr	Pro							
194							570			575							
196	gttctcatg	accgcgagcg	cttaactgcc	aacatttcca	ggatggcagc	tcacgccggt											2143
198	ccccatgaga	ttgcct															2160

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201 <210> SEQ ID NO: 2
 202 <211> LENGTH: 579
 203 <212> TYPE: PRT
 204 <213> ORGANISM: Corynebacterium glutamicum
 206 <400> SEQUENCE: 2

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212 Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 213 20 25 30

216 Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 217 35 40 45

220 Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
 221 50 55 60

224 Glu Leu Ala Val Cys Ala Ala Ser Cys Gly Pro Gly Asn Thr His Leu
 225 65 70 75 80

228 Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
 229 85 90 95

232 Ile Ala Ser His Ile Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln
 233 100 105 110

236 Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
 237 115 120 125

240 Met Val Asn Gly Glu Gln Gly Glu Arg Ile Leu His His Ala Ile
 241 130 135 140

244 Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
 245 145 150 155 160

248 Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
 249 165 170 175

252 Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
 253 180 185 190

256 Ala Leu Val Glu Ala Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys
 257 195 200 205

260 Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
 261 210 215 220

264 Lys Ile Lys Ser Pro Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile
 265 225 230 235 240

268 Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
 269 245 250 255

272 Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
 273 260 265 270

276 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
 277 275 280 285

280 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
 281 290 295 300

284 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
 285 305 310 315 320

288 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
 289 325 330 335

292 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
 293 340 345 350

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296 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
 297 355 360 365
 300 Asn Glu Leu Ala Asp Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met
 301 370 375 380
 304 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
 305 385 390 395 400
 308 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
 309 405 410 415
 312 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
 313 420 425 430
 316 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
 317 435 440 445
 320 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
 321 450 455 460
 324 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 325 465 470 475 480
 328 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 329 485 490 495
 332 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 333 500 505 510
 336 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 337 515 520 525
 340 Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 341 530 535 540
 344 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
 345 545 550 555 560
 348 Gly Val Gly Ala Met Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile
 349 565 570 575
 352 Pro Thr Pro
 356 <210> SEQ ID NO: 3
 357 <211> LENGTH: 875
 358 <212> TYPE: DNA
 359 <213> ORGANISM: Corynebacterium glutamicum
 361 <400> SEQUENCE: 3
 362 tgcgagatgg tgaatgggtgg tgagcagggt gaacgcattt tgcatcacgc gattcagtcc 60
 364 accatggcggt gtaaagggtgt gtcgggtggta gtgattcctg gtgatatacgc taaggaagac 120
 366 gcagggtgacg gtacttattc caattccact atttcttctg gcactcctgt ggtgttcccg 180
 368 gatcctactg aggctgcagc gctgggtggag gcgattaaaca acgctaagtc tgtcaacttg 240
 370 ttctgcgggtg cgggcgtgaa gaatgctcgc ggcagggtgt tggagttggc ggagaagatt 300
 372 aaatcacccga tcgggcatgc gctgggttgtt aagcagtaca tccagcatga gaatccgttt 360
 374 gaggtcggca tgcgtggcct gcttggttac ggcgcctgcg tggatgcgtc caatgaggcg 420
 376 gatctgtga ttcttattggg tacggatttc ctttattctg atttccttcc taaagacaac 480
 378 gttgcggcagg tggatatacaa cggtgcgac attggctcgc gtaccacgggt gaagtatccg 540
 380 gtgaccgggtg atgttgcgtc aacaatcgaa aatatttgc ctcatgtgaa ggaaaaaaaca 600
 382 gatcggtcct tccttgcgtc gatgtcaag gcacacgagc gtaagttgag ctcgggtggta 660
 384 gagacgtaca cacataacgt cgagaagcat gtgcctattc accctgaata cggtgcctct 720
 386 attttgaacg agctggcgga taaggatgcg gtgttactg tggataccgg catgtgcaat 780
 388 gtgtggcatg cgaggatcatcg gaggaatccg gaggaacgc ggcactttgt gggttcattc 840
 390 cgccacggca cgatggctaa tgcgttgccatgc 875

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5

VERIFICATION SUMMARY

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